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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,309B

DATE: 05/02/2002

TIME: 16:51:05

Input Set : A:\10002309SequenceListing.txt
 Output Set: N:\CRF3\05022002\J002309B.raw

3 <110> APPLICANT: WISCONSIN ALUMNI RESEARCH FOUNDATION
 5 <120> TITLE OF INVENTION: E. COLI O157:H7 C1 ESTERASE INHIBITOR-BINDING PROTEIN AND
 METHODS OF USE

7 <130> FILE REFERENCE: 096429-9117
 9 <140> CURRENT APPLICATION NUMBER: 10/002,309B
 C--> 10 <141> CURRENT FILING DATE: 2002-04-19
 12 <150> PRIOR APPLICATION NUMBER: 60/243,675
 13 <151> PRIOR FILING DATE: 2000-10-26
 15 <160> NUMBER OF SEQ ID NOS: 17
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2798
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Unknown
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid

p0157

27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (138)..(2798)
 30 <223> OTHER INFORMATION:
 33 <400> SEQUENCE: 1
 34 tttagaaac aggtgtaaaat atgttataaa aataaccaac gactagtcaa taagtcgctc 60
 36 ctgaaaaaat aaaatataga aatactgtta tatccggctg catgaacact aaaatgaatg 120
 38 agagatggag aacaccg atg aaa tta aag tat ctg tca tgt acg atc ctt 170
 39 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu
 40 1 5 10
 42 gcc cct ctg gcg att ggg gta ttt tct gca aca gct gct gat aat aat 218
 43 Ala Pro Leu Ala Ile Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn
 44 15 20 25
 46 tca gcc att tat ttc aat acc tcc cag cct ata aat gat ctg cag ggt 266
 47 Ser Ala Ile Tyr Phe Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly
 48 30 35 40
 50 tcg ttg gcc gca gag gtg aaa ttt gca caa agc cag att tta ccc gcc 314
 51 Ser Leu Ala Ala Glu Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala
 52 45 50 55
 54 cat cct aaa gaa ggg gat agt caa cca cat ctg acc agc ctg cgg aaa 362
 55 His Pro Lys Glu Gly Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys
 56 60 65 70 75
 58 agt ctg ctg ctt gtc cgt ccg gtg aaa gct gat gat aaa aca cct gtt 410
 59 Ser Leu Leu Leu Val Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val
 60 80 85 90
 62 cag gtg gaa gcc cgc gat gat aat aat aaa att ctc ggt acg tta acc 458
 63 Gln Val Glu Ala Arg Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr

64

95

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5/2/02

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66	ctt tat cct cct tca tca cta ccg gat aca atc tac cat ctg gat ggt	506
67	Leu Tyr Pro Pro Ser Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly	
68	110 115 120	
70	gtt ccg gaa ggt ggt atc gat ttc aca cct cat aat gga acg aaa aag	554
71	Val Pro Glu Gly Gly Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys	
72	125 130 135	
74	atc att aat acg gtg gct gaa gta aac aaa ctc agt gat gcc agc ggg	602
75	Ile Ile Asn Thr Val Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly	
76	140 145 150 155	
78	agt tct att cat agc cat cta aca aat aat gca ctg gtg gag atc cat	650
79	Ser Ser Ile His Ser His Leu Thr Asn Asn Ala Leu Val Glu Ile His	
80	160 165 170	
82	act gca aat ggt cgt tgg gta aga gac att tat ctg ccg cag gga ccc	698
83	Thr Ala Asn Gly Arg Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro	
84	175 180 185	
86	gac ctt gaa ggt aag atg gtt cgc ttt gtt tcg tct gca ggc tat agt	746
87	Asp Leu Glu Gly Lys Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser	
88	190 195 200	
90	tca acg gtt ttt tat ggt gat cga aaa gtc aca ctc tcg gtg ggt aac	794
91	Ser Thr Val Phe Tyr Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn	
92	205 210 215	
94	act ctt ctg ttc aaa tat gta aat ggt cag tgg ttc cgc tcc ggt gaa	842
95	Thr Leu Leu Phe Lys Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu	
96	220 225 230 235	
98	ctg gag aat aat cga atc act tat gct cag cat att tgg agt gct gaa	890
99	Leu Glu Asn Asn Arg Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu	
100	240 245 250	
102	ctg cct gcg cac tgg atc gtg cct ggt tta aac ttg gtg att aaa cag	938
103	Leu Pro Ala His Trp Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln	
104	255 260 265	
106	ggc aat ctg agc ggt cgc cta aat gat atc aag att gga gca ccg ggt	986
107	Gly Asn Leu Ser Gly Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly	
108	270 275 280	
110	gag ctg ttg ttg cat aca att gat atc ggg atg ttg acc act ccc cgg	1034
111	Glu Leu Leu Leu His Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg	
112	285 290 295	
114	gat cgc ttt gat ttt gcc aaa gac aaa gaa gca cat agg gaa tat ttc	1082
115	Asp Arg Phe Asp Phe Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe	
116	300 305 310 315	
118	cag acc att cct gta agt cgt atg att gtt aat aat tat gcg cct cta	1130
119	Gln Thr Ile Pro Val Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu	
120	320 325 330	
122	cac cta aag gaa gtt atg tta cca acc gga gag tta ttg aca gat atg	1178
123	His Leu Lys Glu Val Met Leu Pro Thr Gly Glu Leu Leu Thr Asp Met	
124	335 340 345	
126	gat cca gga aat ggt ggg tgg cat agt ggt aca atg cgt caa aga ata	1226
127	Asp Pro Gly Asn Gly Gly Trp His Ser Gly Thr Met Arg Gln Arg Ile	
128	350 355 360	
130	ggt aaa gaa ttg gtt tcg cat ggc att gat aat gct aac tat ggt tta	1274

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131	Gly	Lys	Glu	Leu	Val	Ser	His	Gly	Ile	Asp	Asn	Ala	Asn	Tyr	Gly	Leu	
132	365				370				375								
134	aat	agt	acc	gca	ggc	tta	ggg	gag	aat	agt	cat	cca	tat	gta	gtt	gcg	1322
135	Asn	Ser	Thr	Ala	Gly	Leu	Gly	Glu	Asn	Ser	His	Pro	Tyr	Val	Val	Ala	
136	380				385				390							395	
138	caa	tta	gcf	gca	cat	aat	agc	cgc	ggt	aat	tat	gct	aat	ggc	atc	cag	1370
139	Gln	Leu	Ala	Ala	His	Asn	Ser	Arg	Gly	Asn	Tyr	Ala	Asn	Gly	Ile	Gln	
140		400				405				410							
142	gtt	cat	ggt	ggc	tcc	gga	ggt	ggg	gga	att	gtt	act	tta	gat	tcc	aca	1418
143	Val	His	Gly	Gly	Ser	Gly	Gly	Gly	Ile	Val	Thr	Leu	Asp	Ser	Thr		
144		415				420				425							
146	ttg	ggg	aat	gag	ttc	agt	cat	gaa	gtt	ggt	cat	aat	tat	ggt	ctt	ggt	1466
147	Leu	Gly	Asn	Glu	Phe	Ser	His	Glu	Val	Gly	His	Asn	Tyr	Gly	Leu	Gly	
148		430				435				440							
150	cat	tat	gta	gat	ggt	tcc	aag	ggt	tct	gta	cat	cgt	agt	gca	gaa	aat	1514
151	His	Tyr	Val	Asp	Gly	Phe	Lys	Gly	Ser	Val	His	Arg	Ser	Ala	Glu	Asn	
152		445				450				455							
154	aac	aac	tca	act	tgg	gga	tgg	gat	ggt	gat	aaa	aaa	cgg	ttt	att	cct	1562
155	Asn	Asn	Ser	Thr	Trp	Gly	Trp	Asp	Gly	Asp	Lys	Lys	Arg	Phe	Ile	Pro	
156	460		465			470				475							
158	aac	ttt	tat	ccg	tct	caa	aca	aat	gaa	aag	agt	tgt	ctg	aat	aat	cag	1610
159	Asn	Phe	Tyr	Pro	Ser	Gln	Thr	Asn	Glu	Lys	Ser	Cys	Leu	Asn	Asn	Gln	
160		480				485				490							
162	tgt	caa	gaa	ccg	ttt	gat	gga	cac	aaa	ttt	ggt	ttt	gac	gcc	atg	gcg	1658
163	Cys	Gln	Glu	Pro	Phe	Asp	Gly	His	Lys	Phe	Gly	Phe	Asp	Ala	Met	Ala	
164		495				500				505							
166	gga	ggc	agc	cct	tcc	tct	gct	gca	aac	cgt	ttc	aca	atg	tat	act	ccg	1706
167	Gly	Gly	Ser	Pro	Phe	Ser	Ala	Ala	Asn	Arg	Phe	Thr	Met	Tyr	Thr	Pro	
168		510				515				520							
170	aat	tca	tcg	gct	atc	atc	cag	cgt	ttt	ttt	gaa	aat	aaa	gct	gtg	tcc	1754
171	Asn	Ser	Ser	Ala	Ile	Ile	Gln	Arg	Phe	Phe	Glu	Asn	Lys	Ala	Val	Phe	
172		525				530				535							
174	gat	agc	cgt	tcc	tcc	acc	ggc	tcc	agc	aag	tgg	aat	gca	gat	acg	cag	1802
175	Asp	Ser	Arg	Ser	Ser	Thr	Gly	Phe	Ser	Lys	Trp	Asn	Ala	Asp	Thr	Gln	
176	540		545			550				555							
178	gaa	atg	gaa	ccg	tat	gaa	cac	acc	att	gac	cgt	gcg	gag	cag	att	acg	1850
179	Glu	Met	Glu	Pro	Tyr	Glu	His	Thr	Ile	Asp	Arg	Ala	Glu	Gln	Ile	Thr	
180		560				565				570							
182	gct	tca	gtc	aat	gag	cta	agt	gaa	agc	aaa	atg	gct	gag	ctg	atg	gca	1898
183	Ala	Ser	Val	Asn	Glu	Leu	Ser	Glu	Ser	Lys	Met	Ala	Glu	Ieu	Met	Ala	
184		575				580				585							
186	gag	tac	gct	gtc	aaa	gtg	cat	atg	tgg	aac	ggt	aac	tgg	aca	aga		1946
187	Glu	Tyr	Ala	Val	Val	Lys	Val	His	Met	Trp	Asn	Gly	Asn	Trp	Thr	Arg	
188		590				595				600							
190	aac	atc	tat	atc	cct	aca	gcc	tcc	gca	gat	aat	aga	ggc	agt	atc	ctg	1994
191	Asn	Ile	Tyr	Ile	Pro	Thr	Ala	Ser	Ala	Asp	Asn	Arg	Gly	Ser	Ile	Leu	
192		605				610				615							
194	acc	atc	aac	cat	gag	gcc	ggt	tat	aat	agt	tat	ctg	ttt	ata	aat	ggt	2042
195	Thr	Ile	Asn	His	Glu	Ala	Gly	Tyr	Asn	Ser	Tyr	Ieu	Phe	Ile	Asn	Gly	

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196	620	625	630	635	
198	gac gaa aag gtc gtt tcc cag ggg tat aaa aag agc ttt gtt tcc gat				2090
199	Asp Glu Lys Val Val Ser Gln Gly Tyr Lys Lys Ser Phe Val Ser Asp				
200	640	645	650		
202	ggt cag ttc tgg aaa gaa cgt gat gtg gtt gat act cgt gaa gcg cgt				2138
203	Gly Gln Phe Trp Lys Glu Arg Asp Val Val Asp Thr Arg Glu Ala Arg				
204	655	660	665		
206	aag cca gag cag ttt ggt gtt cct gtg acg acc ctg gtg ggg tat tac				2186
207	Lys Pro Glu Gln Phe Gly Val Pro Val Thr Thr Leu Val Gly Tyr Tyr				
208	670	675	680		
210	gat ccg gaa ggc acg ctg tca acg tac atc tat cct gcg atg tat ggt				2234
211	Asp Pro Glu Gly Thr Leu Ser Ser Tyr Ile Tyr Pro Ala Met Tyr Gly				
212	685	690	695		
214	gcc tat ggc ttc act tat tcc gat gat agt cag aat cta tcc gat aac				2282
215	Ala Tyr Gly Phe Thr Tyr Ser Asp Asp Ser Gln Asn Leu Ser Asp Asn				
216	700	705	710	715	
218	gac tgc cag ctg cag gtg gat acg aaa gaa ggg cag ttg cga ttc aga				2330
219	Asp Cys Gln Leu Gln Val Asp Thr Lys Glu Gly Gln Leu Arg Phe Arg				
220	720	725	730		
222	ctg gct aat cac cgg gct aac aac act gta atg aat aag ttc cat att				2378
223	Leu Ala Asn His Arg Ala Asn Asn Thr Val Met Asn Lys Phe His Ile				
224	735	740	745		
226	aac gtg cca aca gaa agt cag ccc aca cag gcc aca ttg gtt tgc aat				2426
227	Asn Val Pro Thr Glu Ser Gln Pro Thr Gln Ala Thr Leu Val Cys Asn				
228	750	755	760		
230	aac aag ata ctg gat acc aaa tcg ctc aca cct gcg cca gaa gga ctt				2474
231	Asn Lys Ile Leu Asp Thr Lys Ser Leu Thr Pro Ala Pro Glu Gly Leu				
232	765	770	775		
234	acc tat act gta aat ggg cag gca ctt cca gca aaa gaa aac gag gga				2522
235	Thr Tyr Thr Val Asn Gly Gln Ala Leu Pro Ala Lys Glu Asn Glu Gly				
236	780	785	790	795	
238	tgc atc gtg tcc gtg aat tca ggt aaa cgt tac tgt ttg ccg gtt ggt				2570
239	Cys Ile Val Ser Val Asn Ser Gly Lys Arg Tyr Cys Leu Pro Val Gly				
240	800	805	810		
242	caa cgg tca gga tat agc ctt cct gac tgg att gtt ggg cag gaa gtc				2618
243	Gln Arg Ser Gly Tyr Ser Leu Pro Asp Trp Ile Val Gly Gln Glu Val				
244	815	820	825		
246	tat gtc gac agc ggg gct aaa gcg aaa gtg ctg ctt tct gac tgg gat				2666
247	Tyr Val Asp Ser Gly Ala Lys Ala Lys Val Leu Leu Ser Asp Trp Asp				
248	830	835	840		
250	aac ctg tcc tat aac agg att ggt gag ttt gta ggt aat gtg aac cca				2714
251	Asn Leu Ser Tyr Asn Arg Ile Gly Glu Phe Val Gly Asn Val Asn Pro				
252	845	850	855		
254	gct gat atg aaa aaa gtt aaa gcc tgg aac gga cag tat ttg gac ttc				2762
255	Ala Asp Met Lys Lys Val Lys Ala Trp Asn Gly Gln Tyr Leu Asp Phe				
256	860	865	870	875	
258	agt aaa cct agg tca atg agg gtt gta tat aaa taa				2798
259	Ser Lys Pro Arg Ser Met Arg Val Val Tyr Lys				
260	880	885			

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263 <210> SEQ ID NO: 2
 264 <211> LENGTH: 886
 265 <212> TYPE: PRT
 266 <213> ORGANISM: Unknown
 268 <220> FEATURE:
 269 <223> OTHER INFORMATION: Description of Unknown Organism: E. coli O157:H7 plasmid
 p0157
 271 <400> SEQUENCE: 2
 273 Met Lys Leu Lys Tyr Leu Ser Cys Thr Ile Leu Ala Pro Leu Ala Ile
 274 1 5 10 15
 277 Gly Val Phe Ser Ala Thr Ala Ala Asp Asn Asn Ser Ala Ile Tyr Phe
 278 20 25 30
 281 Asn Thr Ser Gln Pro Ile Asn Asp Leu Gln Gly Ser Leu Ala Ala Glu
 282 35 40 45
 285 Val Lys Phe Ala Gln Ser Gln Ile Leu Pro Ala His Pro Lys Glu Gly
 286 50 55 60
 289 Asp Ser Gln Pro His Leu Thr Ser Leu Arg Lys Ser Leu Leu Leu Val
 290 65 70 75 80
 293 Arg Pro Val Lys Ala Asp Asp Lys Thr Pro Val Gln Val Glu Ala Arg
 294 85 90 95
 297 Asp Asp Asn Asn Lys Ile Leu Gly Thr Leu Thr Leu Tyr Pro Pro Ser
 298 100 105 110
 301 Ser Leu Pro Asp Thr Ile Tyr His Leu Asp Gly Val Pro Glu Gly Gly
 302 115 120 125
 305 Ile Asp Phe Thr Pro His Asn Gly Thr Lys Lys Ile Ile Asn Thr Val
 306 130 135 140
 309 Ala Glu Val Asn Lys Leu Ser Asp Ala Ser Gly Ser Ser Ile His Ser
 310 145 150 155 160
 313 His Leu Thr Asn Asn Ala Leu Val Glu Ile His Thr Ala Asn Gly Arg
 314 165 170 175
 317 Trp Val Arg Asp Ile Tyr Leu Pro Gln Gly Pro Asp Leu Glu Gly Lys
 318 180 185 190
 321 Met Val Arg Phe Val Ser Ser Ala Gly Tyr Ser Ser Thr Val Phe Tyr
 322 195 200 205
 325 Gly Asp Arg Lys Val Thr Leu Ser Val Gly Asn Thr Leu Leu Phe Lys
 326 210 215 220
 329 Tyr Val Asn Gly Gln Trp Phe Arg Ser Gly Glu Leu Glu Asn Asn Arg
 330 225 230 235 240
 333 Ile Thr Tyr Ala Gln His Ile Trp Ser Ala Glu Leu Pro Ala His Trp
 334 245 250 255
 337 Ile Val Pro Gly Leu Asn Leu Val Ile Lys Gln Gly Asn Leu Ser Gly
 338 260 265 270
 341 Arg Leu Asn Asp Ile Lys Ile Gly Ala Pro Gly Glu Leu Leu His
 342 275 280 285
 345 Thr Ile Asp Ile Gly Met Leu Thr Thr Pro Arg Asp Arg Phe Asp Phe
 346 290 295 300
 349 Ala Lys Asp Lys Glu Ala His Arg Glu Tyr Phe Gln Thr Ile Pro Val
 350 305 310 315 320
 353 Ser Arg Met Ile Val Asn Asn Tyr Ala Pro Leu His Leu Lys Glu Val
 354 325 330 335

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/02/2002
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY

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DATE: 05/02/2002

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Input Set \: A:\10002309SequenceListing.txt

Output Set: N:\CRF3\05022002\J002309B.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date